

T340X

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT:

(A) NAME: Burkly, Linda C.
(B) STREET: 34 Winthrop Street
(C) CITY: West Newton
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02165

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(A) NAME: Biogen, Inc.
(B) STREET: Fourteen Cambridge Center
(C) CITY: Cambridge
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02142

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(ii) TITLE OF INVENTION: TREATMENT FOR INSULIN DEPENDENT DIABETES

(iii) NUMBER OF SEQUENCES: 15

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(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 000000 (BGP-151CP)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US94/01456
(B) FILING DATE: 09-FEB-1994

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/029,330
(B) FILING DATE: 09-FEB-1993

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..360

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(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION:/note= "pBAG159 insert: HP1/2 heavy

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chain variable region; amino acid 1 is Glu (E) but
Gln(Q) may be substituted"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

5
GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA 48
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

10
GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT 96
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30

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ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA 144
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
35 40 45

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AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG 192
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
50 55 60

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GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG 240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
65 70 75 80

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CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA 288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

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GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA 336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
100 105 110

40
GGG ACC ACG GTC ACC GTC TCC TCA 360
Gly Thr Thr Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 2:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

50
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
20 25 30

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Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
35 40 45

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
50 55 60

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Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
65 70 75 80

5 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
100 105 110

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Gly Thr Thr Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 3:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..318
 (D) OTHER INFORMATION:/product= "HP1/2 light
 chain variable region"

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- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1
 (D) OTHER INFORMATION:/note= "pBAG172 insert: HP1/2 light
 chain variable region"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

40 AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA 48
 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
 125 130 135

45 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT 96
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
 140 145 150

50 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA 144
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 155 160 165

TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC 192
 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
 170 175 180

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AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT 240
 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
 185 190 195 200

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(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..429

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(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION:/note= "pBAG195 insert: AS heavy chain variable region"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

15	ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly -19 -15 -10 -5	48
20	GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg 1 5 10	96
25	CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GCG TCT GGC TTC AAC ATT Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile 15 20 25	144
30	AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu 30 35 40 45	192
35	GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp 50 55 60	240
40	CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AGC AAC Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn 65 70 75	288
45	CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val 80 85 90	336
50	TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp 95 100 105	384
55	TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser 110 115 120	429

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

38

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
 -19 -15 -10 -5

5 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 1 5 10

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
 15 20 25

10 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
 30 35 40 45

15 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
 50 55 60

Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
 65 70 75

20 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 80 85 90

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
 95 100 105

25 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
 110 115 120

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..386

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..57

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58..386

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION:/note= "pBAG198 insert: VK2
 (SVMDY) light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

39

	ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT	48
	Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
	-19 -15 -10 -5	
5	GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
	Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
	1 5 10	
10	AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG	144
	Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val	
	15 20 25	
15	ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG	192
	Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
	30 35 40 45	
20	CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA	240
	Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg	
	50 55 60	
25	TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
	Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
	65 70 75	
30	CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC	336
	Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser	
	80 85 90	
35	TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG	384
	Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys	
	95 100 105	
40	TG	386

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

	Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
	-19 -15 -10 -5	
50	Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
	1 5 10	
	Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val	
	15 20 25	
55	Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
	30 35 40 45	
	Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg	

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Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
 65 70 75

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Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
 80 85 90

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Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
 95 100 105

(2) INFORMATION FOR SEQ ID NO: 9:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA

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- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1338

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- (ix) FEATURE:
 (A) NAME/KEY: VCAM-1 gene segment
 (B) LOCATION: 1..219
 (D) OTHER INFORMATION: This portion of the sequence
 corresponds, in part, to Exons I, II and III
 nucleotide sequence of Cybulsky et al. Proc. Nat'l.
 Acad. Sci. USA 88: 7861(1991).

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- (ix) FEATURE:
 (A) NAME/KEY: Hinge region
 (B) LOCATION: 220..229
 (D) OTHER INFORMATION: This portion of the sequence
 corresponds, in part, to Fig. 12A in PCT/US92/02050
 and represents the hinge region of Human IgG1 heavy
 chain constant region.

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- (ix) FEATURE:
 (A) NAME/KEY: Heavy chain constant region 2
 (B) LOCATION: 230..338
 (D) OTHER INFORMATION: This portion of the sequence
 corresponds, in part, to Fig. 12A in PCT/US92/02050
 and represents the heavy chain constant region 2 of
 Human IgG1 heavy chain constant region.

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- (ix) FEATURE:
 (A) NAME/KEY: Heavy chain constant region 3
 (B) LOCATION: 339..446
 (D) OTHER INFORMATION: This portion of the sequence
 corresponds, in part, to Fig. 12A in PCT/US92/02050
 and represents the heavy chain constant region 3 of
 Human IgG1 heavy chain constant region.

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

5	ATG CCT GGG AAG ATG GTC GTG ATC CTT GGA GCC TCA AAT ATA CTT TGG Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp 110 115 120 125	48
10	ATA ATG TTT GCA GCT TCT CAA GCT TTT AAA ATC GAG ACC ACC CCA GAA Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu 130 135 140	96
15	TCT AGA TAT CTT GCT CAG ATT GGT GAC TCC GTC TCA TTG ACT TGC AGC Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser 145 150 155	144
20	ACC ACA GGC TGT GAG TCC CCA TTT TTC TCT TGG AGA ACC CAG ATA GAT Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp 160 165 170	192
25	AGT CCA CTG AAT GGG AAG GTG ACG AAT GAG GGG ACC ACA TCT ACG CTG Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu 175 180 185	240
30	ACA ATG AAT CCT GTT AGT TTT GGG AAC GAA CAC TCT TAC CTG TGC ACA Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr 190 195 200 205	288
35	GCA ACT TGT GAA TCT AGG AAA TTG GAA AAA GGA ATC CAG GTG GAG ATC Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile 210 215 220	336
40	TAC TCT TTT CCT AAG GAT CCA GAG ATT CAT TTG AGT GGC CCT CTG GAG Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu 225 230 235	384
45	GCT GGG AAG CCG ATC ACA GTC AAG TGT TCA GTT GCT GAT GTA TAC CCA Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro 240 245 250	432
50	TTT GAC AGG CTG GAG ATA GAC TTA CTG AAA GGA GAT CAT CTC ATG AAG Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys 255 260 265	480
55	AGT CAG GAA TTT CTG GAG GAT GCA GAC AGG AAG TCC CTG GAA ACC AAG Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys 270 275 280 285	528
60	AGT TTG GAA GTA ACC TTT ACT CCT GTC ATT GAG GAT ATT GGA AAA GTT Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val 290 295 300	576
65	CTT GTT TGC CGA GCT AAA TTA CAC ATT GAT GAA ATG GAT TCT GTG CCC Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro 305 310 315	624
70	ACA GTA AGG CAG GCT GTA AAA GAA TTG CAA GTC GAC AAA ACT CAC ACA Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr 320 325 330	672

42

	TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	720
	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	
		335					340					345					
5	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	768
	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	
	350					355					360					365	
10	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	816
	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	
					370					375					380		
15	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	864
	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	
				385					390					395			
20	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGG	GTG	GTC	AGC	GTC	912
	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	
			400					405					410				
	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	960
	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	
		415					420					425					
25	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	1008
	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	
	430					435					440					445	
30	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	1056
	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	
					450					455					460		
35	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	1104
	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	
				465					470					475			
40	AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	1152
	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	
			480					485					490				
	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	1200
	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
		495					500					505					
45	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	1248
	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	
	510					515					520					525	
50	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	1296
	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	
					530					535					540		
55	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA			1338
	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
				545				550						555			

TGAGTGCGG

1347

43

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..23
- (D) OTHER INFORMATION: This corresponds to Kinase
Primer 370-31.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TCGTC GAC AAA ACT CAC ACA TGC C
Asp Lys Thr His Thr Cys
1 5

24

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: This corresponds to Kinase
Primer 370-32.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTAAATGAGT GCGGCGGCCG CCAA

24

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

5 GCGGCCGCGG TCCAACCACC AATCTCAAAG CTTGGTACCC GGGAATTCAG ATCTGCAGCA 60
TGCTCGAGCT CTAGATATCG ATTCCATGGA TCCTCACATC CCAATCCGCG GCCGC 115

10 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 25 (A) NAME/KEY: CDS
(B) LOCATION: 21..41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

30 GAGCTCGAGG CGGCCGCACC ATG CCT GGG AAG ATG GTC GTG 41
Met Pro Gly Lys Met Val Val
1 5

35 (2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

50 AAGTCGACTT GCAATTCTTT TAC 23

(2) INFORMATION FOR SEQ ID NO: 15:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCGACGCGGC CGCG

14

46